

# Alpha Virus nsp1 alignment

## CLUSTAL W (1.82) multiple sequence alignment

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SFV_nsp1      MAAK--VHVDIEADSPFIKSLQKAFPSFEVESLQVTPNDHANARAFSHLATKLTIEQETDK 58
RRV_nsp1      --MK--VTVDVEADSPFLKALQKAFPAFEVESQQVTPNDHANARAFSHLATKLTIEQEVPA 56
ONV_nsp1      -MDS--VYVDIDADSAPFLKALQQAYPEFVEPEKQVTPNDHANARAFSHLAIKLTIEQEIDP 57
VEEV_nsp1     -MEK--VHVDIEEDSPFLRALQRSFPQFEVEAKQVTDNDHANARAFSHLASKLTIEVDP 57
SinV_nsp1     -MEKPVVNVDVDPQSPFVVQLQKSFQFEVVAQVTPNDHANARAFSHLASKLTIELEVPT 59
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SFV_nsp1      DTLILDIGSAPSRMMSTHKYHCVCPMRSAEDPERLDSYAKKLAASGKVLDREIAGKIT 118
RRV_nsp1      NITILDVGSAPARRLMSDHSYHCICPMKSAEDPERLANYARKLAKTAGEVLDKNVSGKIT 116
ONV_nsp1      DSTILDIGSAPARRMMSDRKYHCVCPMRSAEDPERLANYARKLASAAGKVTDKNISGKIN 117
VEEV_nsp1     SDTILDIGSAPARRMYSKHKYHCICPMRCAEDPDRLYKYATKLKKNCKEITDKELDKMK 117
SinV_nsp1     TATILDIGSAPARRMFSEHQYHCVCPMRSPEDPDRMMKYASKLAEKACKITNKNLHEKIK 119
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SFV_nsp1      DLQTVMATPDAESPTFCLHTDVTCTAAEVAVYQDVYAVHAPTSLYHQAMKGVRTAYWIG 178
RRV_nsp1      DLQDVMATPDLESPTFCLHTDETCRTAEVAVYQD---VHAPTSLYHQAMKGVRTVYWIG 173
ONV_nsp1      DLQAVMAVPNMETSTFCLHTDATCKQRGDVAIYQDVYAVHAPTSLYHQAIKGVRVAYWIG 177
VEEV_nsp1     ELAAVMSDPDLETETMCLHDDDESCRYEGQVAVYQDVYAVDGPTSLYHQANKGVRVAYWIG 177
SinV_nsp1     DLRTVLDTPDAETPSLCFHNDVTCNMRAEYSVMQDVY-INAPGTIYHQAMKGVRTLYWIG 178
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SFV_nsp1      FDTTPFMFDALAGAYPTYATNWADEQVLQARNIGLCAASLTEGRLGKLSILRKKQLKPCD 238
RRV_nsp1      FDTTPFMFEVVAGAYPTYSTNWADEQVLQARNIGLCATSLSEGHGKISIMRKKRLRPSD 233
ONV_nsp1      FDTTPFMYNAMAGAYPSYSTNWADEQVLKAKNIGLCSTDLSEGRGKLSIMRGKKLKPCD 237
VEEV_nsp1     FDTTPFMFKNLGAGAYPSYSTNWADETVLTARNIGLCSSDVMERSRRGMSILRKKYLKPSN 237
SinV_nsp1     FDTTQFMFSAMAGSYPAYNTNWADEKVLARNIGLCSTKLSEGRGKLSIMRKKELKPGS 238
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SFV_nsp1      TVMFSVGSTLYTESRKLLRSWHLPSVFHLKGKQSFTCRCDTIVSCEGYVVKKITMCPGLY 298
RRV_nsp1      -RMFSVG-TLYIESRLLKSWHLPSVFHLKGKNSFTCRCDTIVSCEGYVVKKITMSPGTY 291
ONV_nsp1      RVLF SVGSTLYPESRKLLQSWHLPSVFHLKGKLSFTCRCDTIVSCEGYVVKRVTMSPGIY 297
VEEV_nsp1     NVLF SVGSTIYHEKRDLLRSWHLPSVFHLRGKQNYTCRCETIVSCDGYVVKRIAISPGLY 297
SinV_nsp1     RVYF SVGSTLYPEHRASLQSWHLPSVFHLNGKQSYTCRCDTVVSCEGYVVKKITISPGIT 298
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SFV_nsp1      GKTVGAVTYHAEGFLVCKTTDTVKGERVSFPVCTYVPSTICDQMTGILATDVTPEDAQK 358
RRV_nsp1      GKTVGAVTHHAEGFLMCKVTDTVRGERVSFPVCTYVPATICDQMTGILATDVTPEDAQK 351
ONV_nsp1      GKTSYGAVTHHAGGFLMCKTTDTVDGERVSFVSCTYVPATICDQMTGILATEVTPEDAQK 357
VEEV_nsp1     GKPSGYAATMHREGFLCCKVTDTLNGERVSFPVCTYVPATLCDQMTGILATDVSADDAQK 357
SinV_nsp1     GETVGAVTHNSEGFLCCKVTDTVKGERVSFPVCTYIPATICDQMTGIMATDISPDDAQK 358
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SFV_nsp1      LLVGLNQRIVVNGRTQRNTNTMKNYLLPIVAVAFSKWAREYKADLDDEKPLGVRERSLTC 418
RRV_nsp1      LLVGLNQRIVVNGRTQRNTNTMKNYLLPVVAQAFSKWAREAKADMEDEKPLGTRERTLTC 411
ONV_nsp1      LLVGLNQRIVVNGRTQRNTNTMKNYLLPIVAAQAFSKWAKECRKDMEDEKLLGVRERTLTC 417
VEEV_nsp1     LLVGLNQRIVVNGRTQRNTNTMKNYLLPVVAQAFARWAKYKEDQEDERPLGLRDRQLVM 417
SinV_nsp1     LLVGLNQRIVINGRTNRNTNTMQNYLLPIIAQGFSKWAKERKDDLDNEKMLGTRERKLTY 418
               *****:***:*****:*****:*. .:***: * : * :*: ** *:* *.

SFV_nsp1      CCLWAFKTRKMHTMYKKPDTQTIVKVPSEFNSFVPSLWSTGLAIPVRSRIKMLLAKKTK 478
RRV_nsp1      CCLWAFKNHKTHTMYKRPDTQTIVKVPSTFDSFVPSLWSSSLSIGIRQRIKLLLGPKLS 471
ONV_nsp1      CCLWAFRKHKHTTVYKRPDTQSIQKVPAEFDSFVPSLWSSGLSIPLRTRIKWLLSKAPK 477
VEEV_nsp1     GCCWAFRRHKITSYKRPDTQTIIKVNDFHSFVLPRIGSNTLEIGLRTRIRKMLEEHKE 477
SinV_nsp1     GCLWAFRTKKVHSFYRPPGTQTCVKVPASFSAFPMSVWTTSLPMSLRQKLKLALQPKKE 478
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SFV_nsp1      -RELIPVLD-ASSARDAEQEERLEAELTREALPPLVPIAPAETG-VVDVDVEELEYHA 535
RRV_nsp1      -RDLPSGD-RNEAREAEKEAETKEAELTREALPPLVGSNCADD--VDQVDVEELTYRA 527
ONV_nsp1      YEQLPHSGN-AEEAAQAEETDAVEEQEAELTREAMPLQ--ATQDDI-QVEIDVEQLEDRA 533
VEEV_nsp1     PSPLITAED-IQEAKCADEAKEVREAEELRAALPLA--ADFEET-TLEADVLDMLQEA 533
SinV_nsp1     EKLLQVSEELVMEAKAAFEDAQEEARAELREALPPLVADKGIEAAAEVVCEVEGLQADI 538
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SFV_nsp1	GA 537
RRV_nsp1	GA 529
ONV_nsp1	GA 535
VEEV_nsp1	GA 535
SinV_nsp1	GA 540
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